

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2001, 09:44:54 ; Search time 2029.33 Seconds
(without alignments)
12851.804 Million cell updates/sec

Title: US-09-784-340-1
Perfect score: 2759
Sequence: 1 caaccatgcgcacgtcgtt.....ctgcacgcgttactgtagcg 2759

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

BASE COUNT 618 a 406 c 467 g 608 t
ORIGIN

Query Match 32.08; Score 882.8; DB 192; Length 2099;
Best Local Similarity 73.48; Pred. No. 1e-177;
Matches 1173; Conservative 0; Mismatches 412; Indels 13; Gaps 3;

34 catcatgagctgcacgaagcagcttggatcttgccttcagctcctctgtgttg 93
11 CATATGCTGCTGAAAAATGTTGGCGCATTTTCTCTGCGAGCTTGGCGCGG 70
94 ctgtgattctgtggaagctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 153
71 CTGTGATTCGTGACGAAGGTCTCGTGTGCTGTGATATAGCCACGCGTGAATC 130
154 caaggtcattctgaagagctcatgtgagggcattgaagtaagtaagtaagtc 213
131 AAGACTATTTCTTGAGAGAGCTTGAGACGAGGCGACGAGGTAAAGTCTGAAATACC 190
214 aaagcttcgttaattgaactgaactgaacttcgttcattgaattgaagtgatcat 273
191 CA---GTATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 247
274 gccacagagacgaacgaagaaatgaatat-----ttgtgaacctgaactga 324
248 GCTGTATGAAATCGAGACGCTGAGATGCTTAAATGATGATGCAAAATCTGCTGGA 307
325 tgtctgcaagcttcaacctggaactgaactgaactgaactgaactgaactga 384
308 TGTGATTCGAAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
385 aataagaaggaactttaaataatgatgtgtgagagcttatacaatcagaagctta 444
368 AGTAAGTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGA 427
445 gaagctacaaggaacacacacacacacacacacacacacacacacacacac 504
428 CAAGCTACGAGGATGCAATATGATGATGATGATGATGATGATGATGATGATGAT 487
505 cctgaagctgtgagctgtgagctgtgagctgtgagctgtgagctgtgagctgt 564
488 GTTGGTGGAGAGAGAGCTTCAATCCCTTTCTGATATGACACTGAGGTTCAGATGGGCTA 547
565 caatagagagcgaagctgtgaggaacttcacagctcacttcacttcacttcact 624
548 CTACATGAGAAACACTGTGGCCAGCTTCCAAATCTCGTATGATGATGATGATGAT 607
625 gacagagacacagacagacacacacacacacacacacacacacacacacacac 684
608 GAGTGGCTGACAGACAAATATGACCTTCACAGAGAGGGAAGAAATATGATGATGAT 667
685 ttgttgcacacttcagatcagatcagatcagatcagatcagatcagatcagat 744
668 GTTGTGTGAGTACTGGCTCCAGCAATATGACTTGTGATCTGTGGATCAGATTTACAGTGA 727
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925 ttcaagggagagatggtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 984
908 CTCTGGAGACATGCTGTAGTATGATTTTCACTGGGCTCAATGTCAGAAACCTGACAGA 967

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1208 TCAGCTCAGACATGCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1267
1285 aactatgacagaggaagattactgaagccttgaagacacacacacacacacacacacacac 1344
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RESULT 2
AK004971
LOCUS 2573 bp mRNA HTC 08-FEB-2001
DEFINITION Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300012D20, full insert sequence.
ACCESSION AK004971
VERSION AK004971.1 GI:12836559
KEYWORDS CAP trapper.
SOURCE Mus musculus (strain: C57BL/6J) adult male liver cDNA to mRNA, clone:1300012D20.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL MEDLINE 20499374
REFERENCE 3 (sites)
AUTHORS Kono, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,

Db 1162 GAACCAATGGCATCTATGAGGCGATCGACATCGCATTCCTATTGGATTCCTTGT 1221

Qy 1218 ttggtatgaagcttgatgaatagcaccatgaagccaaagagcagctgtagaataa 1277

Db 1222 TTGGGATCAACCTGATTAATTAATTAACCATAGTACCAAGGACGAGCTGTAGAGTGG 1281

Qy 1278 actcaaaactaagaagcgaagattactgagggccttgagaagcagctgtaccgatt 1337

Db 1282 ACTTGTATCAATGTCACACTACAGACCTTCTACGCCCTTGAAGACTGTCAATTAATGACC 1341

Qy 1338 cctcttataaagaatgctatgagattacaagaattcaccatgatacactgtataagc 1397

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Qy 1398 cccatagatgagcagctctctctgacgagattgtgcatgagccacaagaagcgaagc 1457

Db 1402 CCTTGAGCGAGCTGTCTTCTTGATCGAGTATGTCATGGCAACAAGAGGCAAGCAGCACC 1461

Qy 1458 tggcatcagctgagccagcagcctgagctgagcagcagcagcagcagcagcagcagc 1517

Db 1462 TTGCGCCAGCTCTGATGACCTTACCTGCTTCCAGTACACACTCTGTGATGTGAGTGG 1521

Qy 1518 tccctcctacgtgtgtgcaactgctgctatctctgttcaaaaaatgttttatttcc 1577

Db 1522 TCGATTTGCTGT 1581

Qy 1578 gtcaaaaacttaataaactagaagaatagaataa 1611

Db 1582 GCCATTAAGACTGTAACATGAGGAAAGAGAA 1615

RESULT 3

AK002736 1896 bp mRNA HTC 08-FEB-2001

LOCUS AK002736 adult male kidney cDNA, RIKEN full-length enriched library, clone:0610033E06, full insert sequence.

ACCESSION AK002736

VERSION AK002736.1 GI:12832933

KEYWORDS CAP trapper.

SOURCE Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone:0610033E06.

ORGANISM Mus musculus

REFERENCE 1 (sites) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci P. and Hayashizaki Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Methods Enzymol. 303, 19-44 (1999)

REFERENCE 2 (sites) Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M. and Hayashizaki Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20493974

REFERENCE 3 (sites) Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Kitsuwa T., Tashiro H., Itoh M., Kikuchi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe S., Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsui M., Yoneda Y., Muramatsu M., Inoue Y., Tanaka T., RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

REFERENCE 4 (sites) The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.

AUTHORS Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5 (bases 1 to 1896)

AUTHORS Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A., Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F., Imoto A., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno C., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M. and Hayashizaki Y.

TITLE Submitted (10-JUL-2000) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCCGACCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3'] cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA was through one round of normalization to R6 = 5.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGCGCGCCGACCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI, 3' end: XhoI. Host: SOBR.

FEATURES

source Location/Qualifiers

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/strain="C57BL/6J"

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/db_xref="MGD:MGI:1904280"

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/clone="0610033E06"

/sex="male"

/tissue_type="kidney"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

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/db_xref="GI:12832934"

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CDS

BASE COUNT 571 a 361 c 386 g 578 t

ORIGIN

Query Match 22.6%; Score 623; DB 192; Length 1896;

Best Local Similarity 63.3%; Pred. No. 2,1e-122;

Matches 1013; Conservative 0; Mismatches 570; Indels 18; Gaps 3;

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Db 61 TGTGTCTCTGCGAGATAGTGTGCTTCCATCTGTAATGTGGAGAAAGTGTGTGTGT 120

QY 123 ggccctgtacatgaagccattggcttaattgtcaaggtcaatctcagaagctcatagtga 182
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 Db 958 ttctctgtgggtgactgttctcaaatgcttacaagaagaagaagcctatcatctgtctcag 1017
 QY 1011 cccctgtgccaagatccacagaagtgcttctgaggtacaaagaagaagaagaagaagaaga 1070
 Db 1018 cccctgtgccaagatccacagaagtgcttctgaggtacaaagaagaagaagaagaagaaga 1077
 QY 1071 taggagccacactcgtgctgattgattgataccccaagaatgtcttctgtgcatccca 1130
 Db 1078 taggagccacactcgtgctgattgattgataccccaagaatgtcttctgtgcatccca 1137
 QY 1131 aaaccaaagcttatacactcgtgtgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaa 1190
 Db 1138 aaaccaaagcttatacactcgtgtgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaa 1197

QY 1191 gggctccatagtggtggaagctcccatatttggctgatacagctgtgataacatagctcacatga 1250
 Db 1198 gaattccctatgattggcatttcttggtttgagaaacagctgataacatgctccatagtg 1257
 QY 1251 aggcacaaagagcagctgtlgaataaactcaaaactatgacaacagaaatctactga 1310
 Db 1258 tggcacaagagcagctgttactgattgaaatgcaaaacaaatgcaagctgacatgctgca 1317
 QY 1311 gggccttgaagaacagctcaatcagcattccctctataaagaagaatgctatgattacaa 1370
 Db 1318 atccactgagagaaagctatgaaatcccttctatgaaagaaatgctatgcttgcacaa 1377
 QY 1371 gaattacacatgatacactcgtgaagcccttagatgagaagctctctgatacagcttc 1430
 Db 1378 ccaattcaccatgacacagcctatgaaaccccttgacagagctgatttctgctgagatttg 1437
 QY 1431 tcatgcccacaaagagcacaagcagctcgtacatgacatgacacacacacacacacacac 1490
 Db 1438 tcatggccacaaagagcacaagcagctcgtacatgacacacacacacacacacacacac 1497
 QY 1491 agcactactctatagatgtaattgggttccctgctgacacacacacacacacacacacac 1550
 Db 1498 agtaccac 1557
 QY 1551 tgttcaaaaatgttttatttcttctgcaaaaattt---aataaaactagaagaatag 1607
 Db 1558 ttactgttaagctccttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1617
 QY 1608 aaaaagagagatagatccttcccaatcacaagaagacactga 1648
 Db 1618 aagaatgagtagagcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1658

RESULT 4
 A0784447
 LOCUS A0784447 595 bp DNA GSS 03-AUG-1999
 DEFINITION HS_3141.A2.H04-T7c C/T Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate-3141 Col-8 Row-O, DNA sequence.
 ACCESSION A0784447
 VERSION A0784447.1 GI:5692071
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 595)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 JOURNAL MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 3141 Row: O Column: 8
 Seq primer: 17
 Class: BAC ends
 High quality sequence stop: 595.
 Location/Qualifiers
 1..595
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=3141 Col=8 Row=O"
 /clone_lib="CIR Approved Human Genomic Sperm Library D"
 /sex="male"

FEATURES

source

Oy	2165	agttgcctataattccacatcactcatcaagtgttcacatgacctaatcttcgcca	2219
Dd	656	AAGTTGGTGTGCTTCCTCGACCCACCATTAAATGTCGGCCTCATTTTGTGCCA	710
RESULT	6		
LOCUS	Bf689099/c		
DEFINITION	Bf689099	823 bp	mRNA
ACCESSION	60218517/21 NIH_MGC_43	Homo sapiens	EST
VERSION	Bf689099		cdna clone IMAGE:4299880 3',
KEYWORDS	Bf689099.1	GI:11974507	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
JOURNAL	1 (bases 1 to 823)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cga@bs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (ULNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: http://image.lnl.gov Plate: LICM1157 row: 0 column: 17 High quality sequence start: 5 High quality sequence stop: 796 Location/Qualifiers 1..823 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4299880" /clone_1lb="NIH_MGC_43" /tissue_type="normal pigmented retinal epithelium" /lab_host="DH10B (phage-resistant)" /note="Organ: eye; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adapter: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC library." 1"		
FEATURES			
SOURCE			
BASE COUNT	221 a	199 c	164 g
ORIGIN			239 t
Query Match	17.3%; Score 477; DB 168; Length 823; Best Local Similarity 78.0%; Pred. No.2,4e-91;		
Matches	587; Conservative	0; Mismatches	165; Indels 1; Gaps 1
Oy	876	gtaaacctcgcaaaagcttgcctaagaagaatggcaaatgtgccagagtcagggaag	935
Dd	804	GCAAAACCGGCGAACCCCTGCTTAAGAAGGAATGGAAGACTTTGTACAGAGATTCTGGAGANA	745
Oy	936	atgatgatgttgatgtttctctgagggtacactgttcaaattgtaccagaagaagaagcta	995
Dd	744	ATGGTGTTGTGTGTTTCTCTGGGGTCATGTGCTAGTAACTGACAGAAAGAGGCGCA	685
Oy	996	atatatgtcttcacgaccttcccagatccccacagaagaagtgtagtagagtagtaaagaa	1055
Dd	684	ACGTAATTGTCATCAACCTGCGGCCAGATCCCAAAAAGTCTCTGGAGATTTGATGGGA	625
Oy	1056	aaaaccatcacatagagaccaatactcggctgtatgatattgtagataccccaagatgac	1115
Dd	624	ATAAACCGAGATACCTTAGGTTCTCAATTAACCTGGCTGTATTAAGTGAGATACCCCAGAAATGACC	565

Oy	1116	ttttgtgcatcccaaaaacccaacttctatcactcatgttggaataigaaggtcatg	1175
Dd	564	TTTAGGTCATCCAAAGACGACACTTTTATACTCATGGGGGCCCAATGGCATCTACG	505
Oy	1176	aagcattaccagggggtcccctatggtgtagtgtccataattgfgatcacgttgata	1235
Dd	504	AGGCATTCTACCATTGGGATFCCCTATTGGTGSGGATTTCCATTGTGTGGCGATCAACCTGATA	445
Oy	1236	acatatgcacaagaagccaaagaagcagctgtgataaataaacctcaaatgacaa	1295
Dd	444	ACAATGGCTCACATGAAGGCCAGGGAGACAGCTGTTAGAGTGEGACTTCACACATGTGCA	385
Oy	1236	gcgaagattactgaagggtttggaacagtcacttaacgnttctctctataaagaagt	1355
Dd	384	GTAACGACTCTCTCAATCATTATTAAGAAGATTAATTAATGATCTTCAATPAAGAGATG	325
Oy	1356	ctatagaetlctcaagaatccacctgatcaacctgtlaaagccccctagatcgagaactc	1415
Dd	324	TATATCAATTTTCAAGATTTCACATGATCATCAACCATGTAAG-CCCTGGATCGAGCACTCT	266
Oy	1416	tctgatcagaattgtcatgctgcgcacaaagaagcaagcaactgycalcagctgccatg	1475
Dd	265	TCTGGATTGAATTTGTCTATGCGCCACAAGAGAGCTTAACACCTTCGGGTTGCAGCCCAGC	206
Oy	1476	accctcactgtgtccagacactcctaatagtatgtgattgggttctctgtaccgylbg	1535
Dd	205	ACCTCACTCGTTCCAGTACACACTCTTTGGATGTGATTTGGTTCTCTGCTGCTGTGG	146
Oy	1536	caactgcatactctctgtccacaatglttttatcttctctgcacaataattaataa	1595
Dd	145	CACCTGTATTTTATATGCTCACAAAATGTTGTCTGTTTTGTTTGTGSAAGTTCTTGAA	86
Oy	1596	ctagaagaatagaaaaaggaagaatagatcttc	1628
Dd	85	AAGCAAAGAGGAAAAAATGATTATTATTC	53
RESULT	7		
BG249053			
LOCUS	60236182BP1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4470199	EST	13-FEB-2001
DEFINITION	mRNA sequence.		
ACCESSION	BG249053		
VERSION	BG249053.1 GI:12758869		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabsr@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov plate: LHAM10287 row: h column: 08 High quality sequence stop: 661. Location/Qualifiers 1. .671 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4470199" /clone_id="NIH_MGC_89" /tissue_type="hypernephroma, cell line" /lab_host="DH10B (phage-resistant)"		
FEATURES	source		

/note="Organ: kidney; Vector: PCMV-SPORT6; Site_1: NOTI; Site_2: Sali; Cloned unidirectionally; oligo-dt primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."

BASE COUNT 206 a 123 c 153 g 189 t

ORIGIN

Query Match 16.9%; Score 467.4; DB 175; Length 671;
Best Local Similarity 94.2%; Pred. No. 2.6e-89;
Matches 606; Conservative 0; Mismatches 21; Indels 16; Gaps 11;

QY 204 tgaactcaaaagccttcgttaattgaactcaagaagccttcgaattgaattgtg 263
DB 11 TGACTCACTCAAAAGCCCTTCGTTAA-TGACTACAGAGAGCCCTTCGATGAAA--TTAAGG 67
QY 264 tggctccatgcccacagacagacagacagacagacagacagacagacagac 323
DB 68 TGGTCCATATGCCACAGACAGACAGACAGACAGACAGACAGACAGACAG 126
QY 324 atgtcttgcaggccttaacacctgcagctgacgtatataaattgaattgtgtg 383
DB 127 ATGCTTGCAGAGCTTATCACTGCGCATACGTTAATAATTAATGATTTTGTG 186
QY 384 aataagaaggaaacttaaaaaatgctgtgagagccttatacacaacagacgtatga 443
DB 187 AAATTAAGAGAACTTAAATAATGATGTGAGAGCTTATCAATCAAGAGCTTATGA 246
QY 444 agaagctacagagaacacacacacacacacacacacacacacacacacacac 503
DB 247 AGAAGCTACAGAGAAACCACTACAGATGATGCTTATAGACCTGTGATTCCTGTGAG 306
QY 504 acctgctgctgagtgctgctgctgctgctgctgctgctgctgctgctgctg 562
DB 307 ACCTGATGCTGAGTGTGCTGAGTCCCTTTGCTGCTACACTTAATTTTCTGATGAGA 366
QY 563 ggaacatgagaggaagc-gtgggaacattccagctcca-cttccatgtaactgtgc 620
DB 367 GGCATATGAG 426
QY 621 ctatgacagac 676
DB 427 CTAATGACAGAGCTTAACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
QY 677 cttaagcttcttccactctctgattcagacacacacacacacacacacacac 736
DB 487 CTTTACAGTTTGTGCCACTTCTGATTCAGATTCAGACTATCATTTGTGGGGAAGAGTG 546
QY 737 t--ataagtaagcattaggaagccacacacacacacacacacacacacacac 794
DB 547 TCAGTAGTAGAGCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606
QY 795 tatgg-ctaatacagacacacacacacacacacacacacacacacacacacac 836
DB 607 TATGGCTTAATACGAACATAT--GGGATTTGAATTTCCCTCAAC 647

RESULT 8
LOCUS AQ026472 501 bp DNA GSS 17-SEP-1998
DEFINITION HS_3241_A2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo
ACCESSION AQ026472
VERSION AQ026472.1 GI:3617042
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 501)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

TITLE Hood,L.
JOURNAL Sequence-tagged connectors: A sequence approach to mapping and
MEDLINE scanning the human genome
COMMENT Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3241 row: M column: 18
Class: BAC ends
High quality sequence stop: 501.
Location/Qualifiers
1..501
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 135 a 110 c 93 g 160 t 3 others

ORIGIN

Query Match 15.8%; Score 437.2; DB 225; Length 501;
Best Local Similarity 95.4%; Pred. No. 6.8e-83;
Matches 460; Conservative 0; Mismatches 20; Indels 2; Gaps 1;

QY 1372 aattcaacatgatcaacacgttaaaagccctagatcagacagcttcttgatgagttgt 1431
DB 21 ATTCACACCTGATACCTGATACAGCCCTAGATGAGAGAGAGAGAGAGAGAGAG 80
QY 1432 catggccacaagaagagcacaagacacacacacacacacacacacacacac 1491
DB 81 CATGGCCACAAAG 140
QY 1492 gcaactactatagatgtagtgggttcctgctgacacgtgtgcaactgtatattct 1551
DB 141 GCAGTACTATATAGATGATGATGGGTCTGCTGACAGCTGTGAGAGAGAGAGAG 200
QY 1552 gttccaaatgttt 1611
DB 201 GTTCACAAAATGTTTTTATTTTCTGTCGCAAAAATTTTATTAATAAACTAGAAA 260
QY 1612 gagggaatagatcttccaaattcaagaagaacacacacacacacacacacac 1671
DB 261 GAGGGAATAGAGCTTTCCCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 320
QY 1672 ccacatagaatttggtgaacacacacacacacacacacacacacacacacacac 1731
DB 321 CCACATTAATAATTTGTTGAACCTTGCTATTTTCAATATTAATTTGTTATTTACT 380
QY 1732 tagctatatagccttagaatttccatgatcatgagttgtggaatatatcttcttgg 1791
DB 381 TAGCTATATAGCTTAGAATTTCCATGATGATGAGGTGAGATATATCATCTTTGCTT 440
QY 1792 gcaatttccatagtgtagtctactctctctctctctctctctctctctctctct 1851
DB 441 GATTTTCTCTAGAGGCT--TACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 498
QY 1852 tc 1853
DB 499 TC 500

RESULT 9
LOCUS BF688309 746 bp mRNA EST 22-DEC-2000

```

DEFINITION 602185172F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:429880 5',
ACCESSION BF688309
VERSION BF688309.1 GI:11973717
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 746)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaups-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM157 row: 0 column: 17
High quality sequence stop: 707.

FEATURES
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location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:429880"
/clone_1ib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. 1"

BASE COUNT 212 a 158 c 183 g 193 t

Query Match 15.8%; Score 435; DB 168; Length 746;
Best Local Similarity 79.8%; Pired. No. 2e-82;
Matches 574; Conservative 0; Mismatches 140; Indels 5; Gaps 5;

QY 857 ttgttggaagatgacgtctaaacctgcacaagcttgcctaagaagaatggaattttc 916
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DB 3 tttcttgagagactccactgcacaaacccctgccttaagaaatggaagactttt 62
|||||

QY 917 gtccagagttcaggagaagatgatatgtgttctctctggtgacgtttccaatt 976
|||||
DB 63 gtacagagctcttgagagaatgtgtgtgttctctctggggtcaatgctacgtaac 122
|||||

QY 977 gtaccagaagaagaagctaatatcatgtctcagccctgcacagatcccaagaagtg 1036
|||||
DB 123 atgcacagaaagaaagggccacagatgcatcagccctggccagatcccaaaaggtt 182
|||||

QY 1037 ttatggaggtacaaagaaaaaacatccatattgagacccaattcgtctatgat 1096
|||||
DB 183 ctggtgagatttgatggagaaacacagatgactttagctcaatctcggctgataag 242
|||||

QY 1097 ttgatgcccaagaatgctctctgtgcatcccaaaccaaaagctttatcaccaatg 1156
|||||
DB 243 ttgatgcccaagaatgactcttctgagctatcacaagacaaagctttatcaccaatg 302
|||||

QY 1157 ggaatgaatggagctatgaagctattacacatggggtcccatggtggaagtcacata 1216
|||||
DB 303 ggagccaatggactgacgagcaatctaccatggagatccctatggtggatccatttg 362
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QY 1217 ttgtgtatcagctgtgataacatagctccacatgaagcacaagaagcagctgtgaata 1276
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DB 363 tttcccgatcacactgataacattgctcactgaagagcc agggacagctgttagactg 421
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QY 1277 aactcaaaactatgaagaaggaagattactgagggctttgaagaacagtcataccgat 1336
|||||
DB 422 gacttcaacacaaatgtgagatgacagacttgctgaatgcatggaagagatgaatgaat 481
|||||

QY 1337 tctctataaagaagaatgctatgagattatcaagaatcaccatgataacatgtaag 1396
|||||
DB 482 ccttcataataaagaaatgttatgaaattatcaagaatcaatgacatgacagtgtag 541
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QY 1397 cccctgagcagaagctcttgatcgaagtttcataggcccaagaagggccaagac 1456
|||||
DB 542 cccctgagcagaagctcttgatcgaagtttcataggcccaagaagggcttaaacac 601
|||||

QY 1457 ctgagatcagctgcccatacctacacactggttcacagcactctatagatgatgg 1516
|||||
DB 602 cttaggggtgacgcccacga-ctgacactggttccagatcactct-ctgagtgatgg 659
|||||

QY 1517 ttctgtgacctgtgtggcaactgctatattctgttcacaaagtgtttatttc 1575
|||||
DB 660 tt-ctgctgctgtgctgggc-actgtgatattatgctcacaagaatgctgctgttc 716
|||||

RESULT 10
AQ441905 446 bp DNA GSS 31-MAR-1999
LOCUS
DEFINITION HS_5058_B2_B12_SP66 RPCR-11 Human Male BAC Library Homo sapiens
ACCESSION genomic clone Plate=634 Col=24 Row=D, DNA sequence.
AQ441905
VERSION AQ441905.1 GI:4553244
KEYWORDS GSS.
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 446)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCR-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear Genetix (Info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 634 row: D column: 24
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 446.

FEATURES
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1..446
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/db_xref="taxon:9606"
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/clone_1ib="RPCR-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRII. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

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/clone="IMAGE:3934561"

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IS							

DEFINITION	123199 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION	BE0133295
VERSION	BE013295.1 GI:8274259
KEYWORDS	EST.
SOURCE	p1g.
ORGANISM	Sus scrofa
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
AUTHORS	1 (bases 1 to 554) Fahrenkrug,S.C., Fekling,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keeler,J.W.
TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL	Unpublished (2000)
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4356 Fax: 402 762 4390 Email: smiththe@mail.marc.usda.gov Single pass sequencing. Bases called and alt.trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options. PCR primers FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTTCCAGTCACGACG Plate: 50 row: G column: 16 Seq primer: ATTTAGGACACTATAG.
FEATURES	location/qualifiers
source	1..554
	/organism="Sus scrofa"
	/db_xref="taxon:9823"
	/clone_id="MARC 1P1G"
	/tissue_type="pooled"
	/lab_host="DH10B"
	/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
BASE COUNT	150 a 120 c 124 g 160 t
ORIGIN	

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Query Match      14.5%; Score 399.4; DB 162; Length 554;
Best Local Similarity 83.3%; Pred. No. 7.6e-75;
Matches 454; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

OY 1048 caaagaaaaaacacatccacattaggagccaatctcgtcgtatgatgtgatacccca 1107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10 CACACGGGAAGAACCCAGAAACATTGAGGCCAATCTCGCTGTATGATGATGATCCACA 69

OY 1108 gaatgattcttcttgtaaccocaaacaaagatttaacatcattatgtaagaatgg 1167
Db 70 GAATGATCTCTCTGGTCAATCCCAACACGAGCCTTTATTAATCACTGTGGAACCAATGG 129

OY 1168 gatcataaagctattaccatggtgggtcccatatgtgtggagttcccatattgtgtatca 1227
Db 130 GATCATTAAGACTATTATACCATGGATGCCCTATGATGATGGGAATTCACATGTTGGTGATCA 189

OY 1228 gctttataacatagctcacaatgaagggccaaagggacgtgtgagaataaactioaaac 1287
Db 190 GCATGATTAATATTTGGCTGTAAAGGCTAAAGGGGGACACTGTTGAATTAACCTTGACAC 249

OY 1288 tatgaagaaggaagatttactcgaagggttttgaagaacagatcatattaccgattcccttataa 1347
Db 250 AATGACGAGTTCGTGATTCGCTTAATGCTTTGAGGACGACTTTTAACAACCCCTTCCTTAATA 309

OY 1348 agaagatgctatgagattatacaagaattcacatgatcatcaactgttlaaagcccttagatcg 1407
Db 310 AGAAATATCTTATGAAGTTATACAGAAATTCACCATGATATTAACCTTAAAGCCCTTGGAACG 369

OY 1408 agcagttcttcttgatcgaagtttgcattgcgcacaaaggaagcgaagcaccctgcagatcgc 1467
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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[illegible]

	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Reser h Genetics (hinfo@resgen.com). BAC end Web Server: http://www.hnsc.washington.edu
	Plate: 659 row: J column:: 24
	Seq primer: T7
	Class: BAC ends
	High quality sequence stop: 552.
FEATURES	Location/Qualifiers
source	. . 552 "/organism='Homo sapiens' '/db_xref='taxon:9606" '/clone='plate=659 Col=24 Row=J' '/clone.lib='PPCI-11 Human Male BAC Library' '/sex='male' '/note-'Vector: pBACE3; 6; Site.1: EcoRI; Site.2: EcoRI; Male blood DNA was isolated from one randomly chosen dono and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"
BASE COUNT	172 a 111 c 84 g 181 t 4 others
ORIGIN	
Query Match	14.3%; Score 394.8; DB 228; Length 552;
Best Local Similarity	91.8%; Pred. No. 7.3e-74;
Matches 428; Conservative	0; Mismatches 37; Indels 1; Gaps 1
OY 1806	gtcttactccttcctccaccttgtagacaagggatgaataactctcaattttccta 1865
Dd 69	GGGCCCTTCCTCCTTTGTGATCACTTATTAAACAAGGACTTAATAVCWCPAATTTTTGCC TA 128
OY 1866	tctctgatatcacctglttlccaagaagcltaactctaccaaccitaaagtgcataagggtgac 1925
Dd 129	TTCCTCATATGCATGGTTTGTCATGANTGTCACTCACTTCTATAACCTTAAGTAGAGGTGAC 188
OY 1926	cfcgaatacgcatgccgatcccgtgfttgtgacaaaacatfgatgtaaagaagttaaaaaaty 1985
Dd 189	CITTCATATCGCATGATTCCTCGTGTGTTGAACAACAACATGARGVTAAAGAATMAAAAATG 248
OY 1986	taaatlcaaanaatlccaglaaacacacacaaalcaaalgaagcataatgatattagctt 2045
Dd 249	TAAAAVTCACGAAAVTCAGTAAACCACACAAATCAGTTAAGCATTCCTANG-CCTTAGCTT 307
OY 2046	gttatgaagaaabaatattttttttttttaattlaataaagcccccttacatataccag 2105
Dd 308	GTTATGAGAAACATATATGTTTTTATATTTTCATTTTAATAAGCCCCCTTCAATACCAG 367
OY 2106	cattaactcctcagacaatgaattgcttaaaaablagacatagggatcctaactsgaata 2165
Dd 368	CATVACTGATGTCAGACATGAATGTTTAAAAATGACAAATAGAGCATTTACACTCAGAATA 427
OY 2166	gtttcctatattccaagactactatctcagatgtcatalatgcttaacatttcyccatcactt 2225
Dd 428	GTTTCCTATATTTTCACATACCTCATCTAGAGATGTCATGTGCTAATTTCTCCATCAC TC 487
OY 2226	aactgcataatttttgtgtgtcttgatgaataaataagacagtycttia 2271
Dd 488	AACCAACATTTTGTGTGTCCTCGATGATTAATAAGACAGGCCCTICA 533
RESULT 15	
AI118428/c	761 bp mRNA EST OZ-SRP-1998
LOCUS	ue40eo9.x1 Sugeno mouse liver mlia Mus musculus CDNA clone
DEFINITION	IMAGE:1482856.3' similar to gb:X06358 Mouse mRNA for
ACCESSION	UDP-glucuronosyltransferase (MOUSE);,, mRNA sequence.
VERSION	AI118428
KEYWORDS	AI118428.1 GI:3518752
SOURCE	EEST. house mouse, Mus musculus
ORGANISM	Mammalia; Eutheria; Rodentia; Sciuroidea; Muridae; Murinae; Cricetidae; Murini; Mus genus; Mus species; Mus domesticus; Mus musculus; Mus musculus domestica; Mus musculus musculus

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